

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/526, 979A  
Source: IFWP  
Date Processed by STIC: 10/05/2006

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 10/05/2006

PATENT APPLICATION: US/10/526,979A

TIME: 10:09:33

Input Set : A:\fbr0003-100 sequence listing.ST25.txt

Output Set: N:\CRF4\10052006\J526979A.raw

3 <110> APPLICANT: Sutherland, Robert  
 4 Henshall, Susan  
 5 O'Brien, Philippa  
 7 <120> TITLE OF INVENTION: Methods of diagnosis and prognosis of ovarian cancer  
 9 <130> FILE REFERENCE: FBR0003-100  
 11 <140> CURRENT APPLICATION NUMBER: US 10/526,979A  
 12 <141> CURRENT FILING DATE: 2005-03-07  
 14 <150> PRIOR APPLICATION NUMBER: PCT/AU2003/001166  
 15 <151> PRIOR FILING DATE: 2003-09-05  
 17 <150> PRIOR APPLICATION NUMBER: AU 2002951346  
 18 <151> PRIOR FILING DATE: 2002-09-05  
 20 <160> NUMBER OF SEQ ID NOS: 84  
 22 <170> SOFTWARE: PatentIn version 3.3  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 3432  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: homo sapiens  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (94)..(2850)  
 34 <400> SEQUENCE: 1  
 35 gtcagtcctt tcgcgctcct gagccgccgg cgcgccgggc gccccgggaa ttataagta 60  
 37 tttgaccgta ctcaaatgt gcaaggaaga ata atg gaa gcc cct gaa tac ctt 114  
 38 Met Glu Ala Pro Glu Tyr Leu  
 39 1 5  
 41 gat ttg gat gaa att gac ttt agt gat gac ata tct tat tca gtc aca 162  
 42 Asp Leu Asp Glu Ile Asp Phe Ser Asp Asp Ile Ser Tyr Ser Val Thr  
 43 10 15 20  
 45 tca ctc aag acg atc cca gaa ctg tgc cga aga tgt gat acg caa aac 210  
 46 Ser Leu Lys Thr Ile Pro Glu Leu Cys Arg Arg Cys Asp Thr Gln Asn  
 47 25 30 35  
 49 gaa gac aga tca gct tct agc tct agc tgg aat tgt ggc atc tca act 258  
 50 Glu Asp Arg Ser Ala Ser Ser Ser Ser Trp Asn Cys Gly Ile Ser Thr  
 51 40 45 50 55  
 53 ctt att aca aac acg caa aag ccc aca gga atc gct gat gtg tac agt 306  
 54 Leu Ile Thr Asn Thr Gln Lys Pro Thr Gly Ile Ala Asp Val Tyr Ser  
 55 60 65 70  
 57 aag ttc cgc cca gtg aag cgg gtt tcg cca ctg aaa cat cag cca gag 354  
 58 Lys Phe Arg Pro Val Lys Arg Val Ser Pro Leu Lys His Gln Pro Glu  
 59 75 80 85  
 61 act ctg gag aac aat gaa agt gat gac caa aag aac cag aaa gtg gtt 402  
 62 Thr Leu Glu Asn Asn Glu Ser Asp Asp Gln Lys Asn Gln Lys Val Val  
 63 90 95 100

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65 gag tac cag aaa ggg ggt gag tct gac ctg ggc ccc cag cct cag gag      450
66 Glu Tyr Gln Lys Gly Gly Glu Ser Asp Leu Gly Pro Gln Pro Gln Glu
67      105      110      115
69 ctt ggc cct gga gat gga gtg ggc ggc cca cca ggt aag agc tct gag      498
70 Leu Gly Pro Gly Asp Gly Val Gly Gly Pro Pro Gly Lys Ser Ser Glu
71 120      125      130      135
73 ccc agc aca tcg ctg ggt gaa ctg gag cac tac gac ctc gac atg gat      546
74 Pro Ser Thr Ser Leu Gly Glu Leu Glu His Tyr Asp Leu Asp Met Asp
75      140      145      150
77 gag att ctg gat gtg cct tat att aaa tcc agt cag cag ctt gcc tct      594
78 Glu Ile Leu Asp Val Pro Tyr Ile Lys Ser Ser Gln Gln Leu Ala Ser
79      155      160      165
81 ttt acc aag gtg act tca gaa aaa aga att ttg ggc tta tgc aca acc      642
82 Phe Thr Lys Val Thr Ser Glu Lys Arg Ile Leu Gly Leu Cys Thr Thr
83      170      175      180
85 atc aat ggc ctt tct ggc aaa gcc tgc tct aca gga agt tct gag agc      690
86 Ile Asn Gly Leu Ser Gly Lys Ala Cys Ser Thr Gly Ser Ser Glu Ser
87      185      190      195
89 tca tca tcc aac atg gca cca ttt tgt gtt ctt tct ccc gtg aaa agc      738
90 Ser Ser Ser Asn Met Ala Pro Phe Cys Val Leu Ser Pro Val Lys Ser
91 200      205      210      215
93 cct cac ttg aga aaa gca tca gct gtc atc cac gac cag cac aag ctg      786
94 Pro His Leu Arg Lys Ala Ser Ala Val Ile His Asp Gln His Lys Leu
95      220      225      230
97 tcc act gaa gaa acc gag atc tca cct cct ctg gtt aaa tgt ggc tct      834
98 Ser Thr Glu Glu Thr Glu Ile Ser Pro Pro Leu Val Lys Cys Gly Ser
99      235      240      245
101 gca tat gag cct gaa aac cag agt aaa gac ttc cta aac aag aca ttt      882
102 Ala Tyr Glu Pro Glu Asn Gln Ser Lys Asp Phe Leu Asn Lys Thr Phe
103      250      255      260
105 agt gat cct cat ggt cga aaa gtt gag aag aca aca cca gac tgc cag      930
106 Ser Asp Pro His Gly Arg Lys Val Glu Lys Thr Thr Pro Asp Cys Gln
107      265      270      275
109 ctc agg gcc ttc cac cta caa tcc tca gca gca gaa tcc aaa cca gaa      978
110 Leu Arg Ala Phe His Leu Gln Ser Ser Ala Ala Glu Ser Lys Pro Glu
111 280      285      290      295
113 gag cag gtc agt ggc cta aac cgg acc agc tcc caa ggc cca gaa gaa      1026
114 Glu Gln Val Ser Gly Leu Asn Arg Thr Ser Ser Gln Gly Pro Glu Glu
115      300      305      310
117 agg agt gag tat ctg aaa aaa gtg aaa agc atc ttg aac att gtt aaa      1074
118 Arg Ser Glu Tyr Leu Lys Lys Val Lys Ser Ile Leu Asn Ile Val Lys
119      315      320      325
121 gaa gga cag atc tct ctc ctg cca cac cta gct gca gac aat cta gac      1122
122 Glu Gly Gln Ile Ser Leu Leu Pro His Leu Ala Ala Asp Asn Leu Asp
123      330      335      340
125 aaa att cac gac gaa aat gga aac aat cta tta cat att gcg gcg tca      1170
126 Lys Ile His Asp Glu Asn Gly Asn Asn Leu Leu His Ile Ala Ala Ser
127      345      350      355
129 cag gga cac gca gag tgt cta cag cac ctc act tct ttg atg gga gaa      1218

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130 Gln Gly His Ala Glu Cys Leu Gln His Leu Thr Ser Leu Met Gly Glu
131 360 365 370 375
133 gac tgc ctc aat gag cgc aac act gag aag ttg act cca gca ggc ctg 1266
134 Asp Cys Leu Asn Glu Arg Asn Thr Glu Lys Leu Thr Pro Ala Gly Leu
135 380 385 390
137 gcc att aag aat ggt cag ttg gag tgc gta cgc tgg atg gtg agc gaa 1314
138 Ala Ile Lys Asn Gly Gln Leu Glu Cys Val Arg Trp Met Val Ser Glu
139 395 400 405
141 aca gaa gcc att gca gaa ctg agt tgt tct aag gat ttt cca agc ctt 1362
142 Thr Glu Ala Ile Ala Glu Leu Ser Cys Ser Lys Asp Phe Pro Ser Leu
143 410 415 420
145 att cat tac gca ggt tgc tat ggc cag gaa aag att ctt ctg tgg ctt 1410
146 Ile His Tyr Ala Gly Cys Tyr Gly Gln Glu Lys Ile Leu Leu Trp Leu
147 425 430 435
149 ctt cag ttt atg caa gaa cag ggc atc tcg ttg gat gaa gta gac cag 1458
150 Leu Gln Phe Met Gln Glu Gln Gly Ile Ser Leu Asp Glu Val Asp Gln
151 440 445 450 455
153 gat ggc aac agt gcc gtt cac gta gcc tca cag cat ggc tac ctt gga 1506
154 Asp Gly Asn Ser Ala Val His Val Ala Ser Gln His Gly Tyr Leu Gly
155 460 465 470
157 tgc ata cag acc ttg gtt gaa tat gga gca aat gtc acc atg cag aac 1554
158 Cys Ile Gln Thr Leu Val Glu Tyr Gly Ala Asn Val Thr Met Gln Asn
159 475 480 485
161 cac gct ggg gaa aag ccc tcc cag agc gcc gag cgg cag ggg cac acc 1602
162 His Ala Gly Glu Lys Pro Ser Gln Ser Ala Glu Arg Gln Gly His Thr
163 490 495 500
165 ctg tgc tcc agg tac ctg gtg gtg gtg gag acc tgc atg tcg ctg gcc 1650
166 Leu Cys Ser Arg Tyr Leu Val Val Val Glu Thr Cys Met Ser Leu Ala
167 505 510 515
169 tct caa gtg gtg aag tta acc aag cag cta aag gaa caa aca gta gaa 1698
170 Ser Gln Val Val Lys Leu Thr Lys Gln Leu Lys Glu Gln Thr Val Glu
171 520 525 530 535
173 cgt gtc acg ctg cag aac caa ctc caa caa ttt cta gaa gcc cag aaa 1746
174 Arg Val Thr Leu Gln Asn Gln Leu Gln Gln Phe Leu Glu Ala Gln Lys
175 540 545 550
177 tca gag ggc aag tca ctc cct tct tca ccc agt tca cca tcc tca cct 1794
178 Ser Glu Gly Lys Ser Leu Pro Ser Ser Pro Ser Ser Pro Ser Ser Pro
179 555 560 565
181 gcc tcc aga aag tcc cag tgg aaa tct cca gat gca gat gat gat tct 1842
182 Ala Ser Arg Lys Ser Gln Trp Lys Ser Pro Asp Ala Asp Asp Asp Ser
183 570 575 580
185 gta gcc aaa agc aag cca gga gtc caa gag ggg att cag gtt ctt gga 1890
186 Val Ala Lys Ser Lys Pro Gly Val Gln Glu Gly Ile Gln Val Leu Gly
187 585 590 595
189 agc ctg tca gcc tcc agc cgg gct aga ccc aaa gca aaa gat gaa gat 1938
190 Ser Leu Ser Ala Ser Ser Arg Ala Arg Pro Lys Ala Lys Asp Glu Asp
191 600 605 610 615
193 tct gat aaa atc tta cgc cag tta ttg gga aag gaa atc tca gaa aat 1986
194 Ser Asp Lys Ile Leu Arg Gln Leu Leu Gly Lys Glu Ile Ser Glu Asn

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195		620		625		630	
197	gtc tgc acc cag gaa aaa ctg tcc ttg gaa ttc cag gat gct cag gct						2034
198	Val Cys Thr Gln Glu Lys Leu Ser Leu Glu Phe Gln Asp Ala Gln Ala						
199		635		640		645	
201	tcc tct aga aat tct aaa aag atc cca ctg gag aag agg gaa ctg aag						2082
202	Ser Ser Arg Asn Ser Lys Lys Ile Pro Leu Glu Lys Arg Glu Leu Lys						
203		650		655		660	
205	tta gcc agg ctg aga cag ctg atg cag agg tca ctg agt gag tct gac						2130
206	Leu Ala Arg Leu Arg Gln Leu Met Gln Arg Ser Leu Ser Glu Ser Asp						
207		665		670		675	
209	aca gac tcc aac aac tct gag gac ccc aag act acc cca gtg agg aag						2178
210	Thr Asp Ser Asn Asn Ser Glu Asp Pro Lys Thr Thr Pro Val Arg Lys						
211	680		685		690		695
213	gct gac cga cca agg ccg cag ccc att gta gaa agc gta gag agt atg						2226
214	Ala Asp Arg Pro Arg Pro Gln Pro Ile Val Glu Ser Val Glu Ser Met						
215		700		705		710	
217	gac agc gca gaa agc ctg cac ctg atg att aag aaa cac acc ttg gca						2274
218	Asp Ser Ala Glu Ser Leu His Leu Met Ile Lys Lys His Thr Leu Ala						
219		715		720		725	
221	tca ggg gga cgc agg ttt cct ttc agc atc aag gcc tcc aaa tcc ctg						2322
222	Ser Gly Gly Arg Arg Phe Pro Phe Ser Ile Lys Ala Ser Lys Ser Leu						
223		730		735		740	
225	gat ggc cac agc cca tct ccc acc tca gag agc agc gaa cca gac tta						2370
226	Asp Gly His Ser Pro Ser Pro Thr Ser Glu Ser Ser Glu Pro Asp Leu						
227		745		750		755	
229	gaa tcc cag tat cca ggc tca ggg agt att cct cca aac cag ccc tct						2418
230	Glu Ser Gln Tyr Pro Gly Ser Gly Ser Ile Pro Pro Asn Gln Pro Ser						
231	760		765		770		775
233	ggt gac cct cag cag ccc agc cct gac agt act gct gcc cag aaa gtt						2466
234	Gly Asp Pro Gln Gln Pro Ser Pro Asp Ser Thr Ala Ala Gln Lys Val						
235		780		785		790	
237	gcc aca agt ccc aag agt gcc ctc aag tct cca tct tcc aag cgt agg						2514
238	Ala Thr Ser Pro Lys Ser Ala Leu Lys Ser Pro Ser Ser Lys Arg Arg						
239		795		800		805	
241	aca tct cag aac tta aaa ctg aga gtt acc ttt gag gag cct gtg gtg						2562
242	Thr Ser Gln Asn Leu Lys Leu Arg Val Thr Phe Glu Glu Pro Val Val						
243		810		815		820	
245	cag atg gag cag cct agc ctt gaa ctg aat gga gaa aaa gac aaa gat						2610
246	Gln Met Glu Gln Pro Ser Leu Glu Leu Asn Gly Glu Lys Asp Lys Asp						
247		825		830		835	
249	aag ggc agg act ctc cag cgg acc tcc aca agt aac gaa tcg ggg gat						2658
250	Lys Gly Arg Thr Leu Gln Arg Thr Ser Thr Ser Asn Glu Ser Gly Asp						
251	840		845		850		855
253	caa ctg aaa agg cct ttt gga gcc ttt cga tct atc atg gag aca cta						2706
254	Gln Leu Lys Arg Pro Phe Gly Ala Phe Arg Ser Ile Met Glu Thr Leu						
255		860		865		870	
257	agt ggc aac caa aac aat aat aat aac tac cag gca gcc aac cag ctg						2754
258	Ser Gly Asn Gln Asn Asn Asn Asn Asn Tyr Gln Ala Ala Asn Gln Leu						
259		875		880		885	

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261 aaa acc tct aca ttg ccc ttg acc tca ctt ggg agg aag aca gat gcc      2802
262 Lys Thr Ser Thr Leu Pro Leu Thr Ser Leu Gly Arg Lys Thr Asp Ala
263      890      895      900
265 aag gga aac cct gcc agc tcc gct agc aaa gga aag aat aag gca gca      2850
266 Lys Gly Asn Pro Ala Ser Ser Ala Ser Lys Gly Lys Asn Lys Ala Ala
267      905      910      915
269 taatgacatc aataaaaaaa tgaagaaatc ctacagcata aagcacattg ctgagccaga      2910
271 gtcaaaagaa ctcttcttgt aaatcacttt ttaaattttc tctcactgat gccctttgga      2970
273 aattattgga aatttctgga ctatcctctt tggaaagaga accatgaaaa caatgcctca      3030
275 ccagcagaag aacagaatat caggatgcct taaattttata gtagtagact gtaaaagatt      3090
277 cattttgggg tgatatctgt atatataact tgttttttta aaagatgccg tttaaaagca      3150
279 tgattgggaa aatgtacgtt ttttaagagt agattgattc accctaccca caggacattc      3210
281 accaagccac tgataccatt ttatatattca tcaattgcac gagtatttgc taatgttgat      3270
283 tgaacctccc tttcccata atgtgggcag atttggctca gctccttcat gagatcaggt      3330
285 cagtgggtatt gtttctgtca agagtgtttt ttctgtcatt tctacttttt gtataaagga      3390
287 aataaaacaa tgtaacagc caaaaaaaaa aaaaaaaaaa aa      3432
290 <210> SEQ ID NO: 2
291 <211> LENGTH: 919
292 <212> TYPE: PRT
293 <213> ORGANISM: homo sapiens
295 <400> SEQUENCE: 2
297 Met Glu Ala Pro Glu Tyr Leu Asp Leu Asp Glu Ile Asp Phe Ser Asp
298 1      5      10      15
301 Asp Ile Ser Tyr Ser Val Thr Ser Leu Lys Thr Ile Pro Glu Leu Cys
302      20      25      30
305 Arg Arg Cys Asp Thr Gln Asn Glu Asp Arg Ser Ala Ser Ser Ser Ser
306      35      40      45
309 Trp Asn Cys Gly Ile Ser Thr Leu Ile Thr Asn Thr Gln Lys Pro Thr
310      50      55      60
313 Gly Ile Ala Asp Val Tyr Ser Lys Phe Arg Pro Val Lys Arg Val Ser
314 65      70      75      80
317 Pro Leu Lys His Gln Pro Glu Thr Leu Glu Asn Asn Glu Ser Asp Asp
318      85      90      95
321 Gln Lys Asn Gln Lys Val Val Glu Tyr Gln Lys Gly Gly Glu Ser Asp
322      100      105      110
325 Leu Gly Pro Gln Pro Gln Glu Leu Gly Pro Gly Asp Gly Val Gly Gly
326      115      120      125
329 Pro Pro Gly Lys Ser Ser Glu Pro Ser Thr Ser Leu Gly Glu Leu Glu
330      130      135      140
333 His Tyr Asp Leu Asp Met Asp Glu Ile Leu Asp Val Pro Tyr Ile Lys
334 145      150      155      160
337 Ser Ser Gln Gln Leu Ala Ser Phe Thr Lys Val Thr Ser Glu Lys Arg
338      165      170      175
341 Ile Leu Gly Leu Cys Thr Thr Ile Asn Gly Leu Ser Gly Lys Ala Cys
342      180      185      190
345 Ser Thr Gly Ser Ser Glu Ser Ser Ser Asn Met Ala Pro Phe Cys
346      195      200      205
349 Val Leu Ser Pro Val Lys Ser Pro His Leu Arg Lys Ala Ser Ala Val
350      210      215      220

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:52; N Pos. 393

**VERIFICATION SUMMARY**

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Input Set : A:\fbr0003-100 sequence listing.ST25.txt

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L:8747 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:52  
L:8769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:360